

SEQUENCE LISTING

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 -- HE, Jiangyan
 YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
 TRANSGENIC ORNAMENTAL FISH

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<170> PatentIn Ver. 2.0

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His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys																	
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Gly His Pro Phe 65	Ile Met Thr Val 70	Gly Cys Val Ala 75	Gly Asp Glu Glu 80
Ser Tyr Asp Val 85	Phe Lys Asp Leu 90	Phe Asp Pro Val 95	Ile Ser Asp Arg 95
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Glu Asn Leu Lys 115	Gly Gly Asp Asp 120	Leu Asp Pro Asn 125	Tyr Phe Leu Ser 125
Ser Arg Val Arg 130	Thr Gly Arg Ser 135	Ile Lys Gly Tyr 140	Pro Leu Pro Pro 140
His Asn Ser Arg 145	Gly Glu Arg Arg 150	Ala Val Glu Lys 155	Leu Ser Val Glu 160
Ala Leu Ser Ser 165	Leu Asp Gly Glu 170	Phe Lys Gly Lys 175	Tyr Tyr Pro Leu 175
Lys Ser Met Thr 180	Asp Asp Glu Gln 185	Glu Gln Leu Ile 190	Ala Asp His Phe 190
Leu Phe Asp Lys 195	Pro Val Ser Pro 200	Leu Leu Leu Ala 205	Ala Gly Met Ala 205
Arg Asp Trp Pro 210	Asp Ala Arg Gly 215	Ile Trp His Asn 220	Glu Asn Lys Ala 220
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Leu Gln Arg Ile 260	Glu Glu Ile Phe 265	Lys Lys His Asn 270	His Gly Phe Met 270
Trp Asn Glu His 275	Leu Gly Phe Val 280	Leu Thr Cys Pro 285	Ser Asn Leu Gly 285
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His Ala Lys Phe 305	Glu Glu Ile Leu 310	Thr Arg Leu Arg 315	Leu Gln Lys Arg 320
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Ser Asn Ala Asp 340	Arg Ile Gly Ser 345	Ser Glu Val Glu 350	Gln Val Gln Cys 350

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Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
115 120 125
Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
130 135 140
Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
145 150 155 160
Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
165 170 175
Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
180 185 190
Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
195 200 205
Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
210 215 220
Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
225 230 235 240
Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
245 250 255
Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
260 265 270
Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
275 280 285
Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
290 295 300
Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
305 310 315

<210> 7
<211> 2241
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (2103)..(2108)

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<220>
<221> primer_bind
<222> (2221)..(2241)
<223> CK2

<220>
<221> misc_feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttccttc tacttttgac gtccttttaa gagcttgtgc atgaaagcag atttggagct 60
gattactcat ctcaaacacc catacaaagg gatgattgcc gtaccatgat ctcacacctt 120
tcacacctgg tttatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180
cagtgtctggc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240
aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggc cattaaatac 300
tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
gtgtgtgaag taacaaatga caaatactca aactattgta attaagtagt ttttctcaga 420
aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttccttg agtacatttt 480
tagtgcagtg ttggtacttt tatttcactt ccttccttca acctgcagtc actactttat 540
ttattcttgt ctatgtggat tagacaaatc agtcctgtga ttctgttcca atcaaattgc 600
acatagaagg taaatcacat cataatgaac taccttaaga catgggcat ttataattgc 660
agcaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaacccag 720
agactgctta gatgcatgtc actgatgaga agatgatgga tgtttactgt atgatgaccg 780
aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcgta gggtgacgtt 840
gtacccaac gcagtgggga cgttgcatth tgtttagaaa tgaaaattag gttgacgtca 900
gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960
ctaagatgt tacagcttga tgttatgcgg atgttacctt tatgacgtct atcagacgtt 1020
ggattatggt tgccatacct gatgaataaa tgtcattatt tgacgttggt ttaagatgtt 1080
ggttcgacat tggattttgg tcgctttcca acacaacct aatccaccaa atattaactt 1140
cctatgacat cgttattgga cgtcaaaata acaatatcct tagatgctgg ctgactttg 1200
aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260
tgctgggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320
taaatgcac agcttttcac agcataatac tcactactta ctactcttga gtacttttaa 1380
aaaagctact tttcactcat actttgagta atatttaca ctgatacttt tactcgcaact 1440
acatttttag gcatgtattg atatttttac tatgattttt cagtactctt tccactactg 1500
cagccctccc catacataat cgtatgttta cacatatggt ggagtttaga gccataatct 1560
acattagctt tgttagccgc tagcattact gtgcagaatt gtgtgtgtgc acattttcca 1620

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atatcaatac agaaggaaac tgtgttcctt gttcccttgt aaatctcaac aatgcaactg 1680
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaag tgaatggaaa 1740
 aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800
 taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgcgtgg 1860
 cagatggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
 ctcaagcctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
 caacatttat ctaccactt tctctctgta cctgtctaac aggtaggggtg tgtgtgagag 2040
 tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagt 2100
 tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
 tgagcaacct cctccactca ctctctctc agagagcact ctctacctc cttctcagca 2220
 actcaaagac acaggatccg g 2241

<210> 8
 <211> 1456
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA_signal
 <222> (1389)..(1394)

<220>
 <221> primer_bind
 <222> (1433)..(1456)
 <223> MCK2

<220>
 <221> misc_feature
 <222> (1428)..(1453)
 <223> Identical to the 5' MCK cDNA

<400> 8
 gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
 tgtggcttaa tcttggtga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
 gcatgtgcac catgacaggc ctgttattca cacttgggtgc catgttggag actgttcggc 180
 cagctatagt tttcttcaca ggtcctggg tcacctaatg tcacaaggaa gaaacatgtt 240
 acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
 ttacagctta aaagattgct agacagaaaa accaggaggg ggttttccca taatatccag 360
 tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
 gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
 acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
 taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
 aagtcaatgg gtcttcacgc attttttcaa tataccttac tttgagttca aaagaaaaac 660

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acatctcaaa taggtttgag gttgaataaa ctttttcat tttggggtgg actatcccta 720
 attatttgac acttaagatt tatagtaaatt ctttttatag actttctccc cttattaaac 780
 atggttgaat ttatcttcat gtttatgtct gggttggtct tttttgaaaa gatttccctg 840
 tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
 tcataacaac tcagattgat gccctttcac cctcagtga taaatatggc gtctgacatg 960
 agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgcac 1020
 ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggctgacac 1080
 gcgcacttct gatatctgtg gtatgtttgg caaaagtgtc gctcagcctt ttttagcatgg 1140
 cagatcctcc acatcccatc acccctcctt caacctattc cctcctggaa agctatgtat 1200
 ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
 catctaggat gcctggggcc taaattgaag cttttcttac actaaacagg gcataagaga 1320
 ccagcgccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcaggg 1380
 gctagaggta tatatatoca aatcaaactc ttcttgcttg ggtgaccctt atttcggctt 1440
 ggtgaacagg atccgg 1456

<210> 9
 <211> 2205
 <212> DNA
 <213> Danio rerio

<220>
 <221> primer_bind
 <222> (2179)..(2205)
 <223> ARP2

<220>
 <221> misc_feature
 <222> (2153)..(2199)
 <223> Identical to the 5' ARP cDNA

<220>
 <221> intron
 <222> (792)..(2152)

<220>
 <221> misc_feature
 <222> (775)..(791)
 <223> Identical to the 5' ARP cDNA

<400> 9
 atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60
 attttaattt gtgttgatata attttacatt ttgtaagtat tatttttata aaaaatatat 120
 agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
 gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
 tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
 agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggtc aattcattaa 360

aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggtgttg ttagaagga tacatctgcg gccgaaagt aacgggaact 480
attt-acattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatgc 600
tatattgacc gcagctgtat ccttttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcatt ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgcgcgtct. tgtggcggtt tcttaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc atttttagtga aatattctta agccactaag ttaaaatttg 1200
tcaatcacat ataattgtgt ttatgtttta ttgagtcac cataccaggt aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaagttaa tcttaagggt gtaaaggctc acccaaaaga caattcacgc tcaagtgttt 1380
tcaaacttta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtgttca ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgacg tgcttgttcg tcgttccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctgggtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttha caaacagtaa ttcataattt gtcatttaat 2100
aagatgcaca caaggcaggt gtaaaagtat tgcttgtgtt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gttcaccgat ccttgaagg gatcc 2205

<210> 10

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
— gene specific primer

<400> 10
cgctggagta agagatagac ctgg 24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
gene specific primer

<220>
<221> misc_feature
<222> (1)..(6)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 11
ccggatcctg tgtctttgag ttgctg 26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 12
ccggatcctt gggatcagat cctg 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc_feature

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<222> (3)..(8)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa

24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc

25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca

26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<400> 16
gttcattcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c

51

<210> 17
<211> 10

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<220>

<223> n is a dideoxycytidine

<400> 17
gaattcaagn

10

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 18
gttcattcttt acaagctagc g

21

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 19
tcctgaacaa tgctgtggac

20

<210> 20

<211> 1392

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (42)..(551)

<220>

<221> primer_bind

<222> (6)..(28)

<223> M2

<220>

<221> primer_bind

<222> (23)..(45)

<223> M1

<220>

<221> polyA_signal

<222> (797)..(802)

<220>

<221> polyA_signal

<222> (1351)..(1357)

<400> 20

ctcttcttga tcttcttaga cttcacacat accgtctcga c atg gca ccc aag aag 56

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Met Ala Pro Lys Lys
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
 Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
 — 10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
 Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
 25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
 Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
 40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
 Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
 55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
 Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
 70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
 Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
 90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
 Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
 105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
 Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
 120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
 Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
 135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
 Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
 150 155 160 165

gag aag gag gag taa acaaccttgg aatcaagaaa acgaagagaa gaacatgcat 591
 Glu Lys Glu Glu
 170

cctcacagct taatctccag tctgttctct ggccttctct aacttttgtt tttccttct 651
 ccctttcttg ctttctacca tctgtgttac tccaagcact tacactctcc atcttaccaa 711
 agacttctct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771
 cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831
 ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891
 cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951
 tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011
 aagaagcacg atggagtgat ctactctat aatagaggaa ccagtcatca ttctcatttc 1071

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ctcctctggt ggttgactaa aaagagaaa agaaaatgag ggttttgtgc tgagtgagtt 1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251
cctctctctc atttctctgt ccactctttc tttttctttt tttctttttt gctttctgca 1311
tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg 1371
aataaaaaaa aaaaaaaaaa a 1392

<210> 21
<211> 169
<212> PRT
<213> Danio rerio

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1 5 10 15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
20 25 30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
35 40 45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
50 55 60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65 70 75 80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
85 90 95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
100 105 110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
115 120 125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
130 135 140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145 150 155 160
Ile Thr His Gly Glu Glu Lys Glu Glu
165

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)

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<223> E-box, canntg

<220>
<221> enhancer
<222> (452)..(457)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1095)..(1100)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1278)..(1283)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1362)..(1367)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1385)..(1390)
<223> E-box, canntg

<220>
<221> enhancer
<222> (523)..(532)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (606)..(615)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (697)..(706)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1490)..(1499)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1640)..(1649)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1956)..(1965)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<223> Transcription start site at residue 2012

<220>
<221> primer_bind
<222> (2032)..(2054)
<223> M2

<220>
<221> misc_difference
<222> (2027)..(2054)
<223> Identical to the 5' MLC2f cDNA

<400> 22
tgcattgcctg gcagggtccac tctagaggac tactagtcac atgcgattct gaacaatgct 60
gtggacagct tgaattcaat tcgccacaga ggaatgagcc accaactcat ccagtgtatt 120
ttttatgcag cggatgcccc tccagttgca accctacact gggaaacacc caaatctgtc 180
ttttaaatta atatttttaa taggaagcta tggtatattt gtgcatatac attagattag 240
tcagtacact ctcagaaata aatgggtccgc aagctgtcac tgcggtgcta ccttttcaaa 300
aggtacatat ttgtacttaa aggggtccata ttgatacctc aaaagtatat attagtgcct 360
aaaaatttta agagaaacac ttttgtactt tttaggtact aatatatacc cttgagggtt 420
tattatggac ctttaaggta caaattttta tcatttggaa aggtaccacc ccagtgcacg 480
ctcacgcctt ttatttctga gagtgaagct aaatctggag cttatttaac aaaataactt 540
atgataacgg tccaaaaact actacacca tatttatatg ttattgaaaa atattaaata 600
caaatttata aacaggggaa aatcaagaga agcaaaacaa tggaaaaaaa ttagttcaaa 660
attttaggtg tgtaattttt ttgttgcaat atttagcttt atttaaattg ttttatcttt 720
caattttgtg actaaaatat tattttaata aatatagctg tttaataaat ctgttttgtt 780
taaattgcacc aaaatacatt gcctatatct actgagagat ggagaaaaat attcattttc 840
aaaatgggct gtactcaatt actctaagca ctgtaattat ctgtttttct aggtactgta 900
aaataatgct aatcttaaac aattttggaa caagcaggag caaaacaagc cgacagactc 960
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